

Please replace claim 8 with the following amended claim

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8. (Amended) The method of claims 1, 2, or 3 wherein said microbe inhabiting a host organism is an intracellular pathogen, wherein said host organism in step (a) has a pathogenic condition, and wherein said database of host organism genomic sequences in step (b) comprises genomic sequences of a plurality of host organisms not having said pathogenic condition.

#### REMARKS

##### Elections under the Restriction Requirement:

In response to the Restriction Requirement, Applicants hereby ELECT, with traverse, Group I, claims 1-7, 10-18, 23-26, 29-31, and 50-61.

It is noted in the Office Action that Groups I and II list claims in common, based on the multiple dependency of the claims. Applicants disagree with the separation of Group II away from Group I because Group II claims have all the limitations of Group I. To expedite prosecution Applicants have amended Group II claims to be dependent upon Group I.

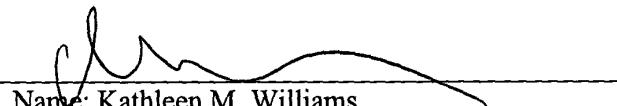
##### Ammended Claim:

Applicants submit that the amended claim is supported throughout the specification. Applicants submit that the claims of Group I are written to identification of "a microbe inhabiting a host organism" and submit that "a microbe inhabiting a host organism" can be either an intracellular or an extracellular pathogen. Since the claims of Group II are written to identification of "an intracellular pathogen", the Applicants have amended independent claim 8 of Group II to be dependent upon independent claims 1, 2, or 3 of Group I. Thus, Applicants

submit that the amended claim and its' dependents thus fall within the methods of Group I as elected.

Respectfully submitted,

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Version of amended claims marked to show changes:

8. The [A] method of claims 1, 2, or 3 [using a computer system to identify an] wherein said microbe inhabiting a host organism is an intracellular pathogen, wherein said host organism in step (a) has a pathogenic condition, and wherein said database of host organism genomic sequences in step (b) comprises genomic sequences of a plurality of host organisms not having said pathogenic condition. [comprising the steps of:]

- [a) obtaining sequence information from at least one host organism having a pathogenic condition;
- b) identifying sequences from said at least one host organism which are not found in a plurality of host organisms not having said pathogenic condition;
- c) comparing said sequences identified in step (b) with a plurality of sequences in a database of host genomic sequences; and
- d) eliminating identified sequences which match said host genomic sequences, wherein any remaining sequences are identified as candidate pathogen sequences.]